AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the application.

1.-85. (Cancelled)

86. (Currently Amended) A method ~~Method~~ for detecting bacteria in an analytical sample, comprising the step of bringing the analytical sample into contact with ~~a~~ an added nucleic acid or a combination of added nucleic acids ~~according to Claim 75~~, and detecting suitable hybrid nucleic acids comprising the added nucleic acid and bacterial nucleic acid, wherein the one or more added nucleic acids are selected from:

a) nucleic acid molecules comprising at least one sequence with any of SEQ ID NOs: 1 to 530 and/or a sequence from position 2667 to 2720, 2727 to 2776, 2777 to 2801, 2801 to 2832, 2857 to 2896, 2907 to 2931, 2983 to 2999 and/or 3000 to 3032 according to SEQ ID NO: 1; or nucleic acids which are homologous or at least 70% identical with them;

b) nucleic acid molecules which hybridize specifically with a nucleic acid according to a);

c) nucleic acid molecules which exhibit 70% identity with a nucleic acid according to a) or b); and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

87. (Currently Amended) The method of claim ~~Method for detecting bacteria in an analytical sample of Claim~~ 86, wherein the bacteria are enterobacteria.

88. (Currently Amended) The method of claim ~~Method according to Claim~~ 86, wherein ~~characterized in that~~ the process involves a PCR amplification of the nucleic acid to be detected.

89. (Currently Amended) The method of claim ~~Method according to Claim~~ 86, wherein ~~characterized in that~~ the process involves a Southern Blot hybridization.

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90. (Currently Amended) A method ~~Method~~ for detecting bacteria in an analytical sample, comprising the step of bringing the analytical sample into contact with ~~a nucleic acid or~~ a combination of nucleic acids ~~according to Claim 82~~, and detecting suitable hybrid nucleic acids comprising the ~~added~~ combination of nucleic acids and bacterial nucleic acid, wherein the combination of nucleic acids comprises a combination of at least 2 nucleic acid molecules, selected from:

a) a combination of at least one DNA molecule which is shortened in comparison with the sequence SEQ ID NO: 1, position 2571 to 2906, and at least one DNA molecule which is shortened or not shortened in comparison with the transcribed spacer between the 23 S and 5 S genes corresponding to position 2907 to 2999 in SEQ ID NO: 1, or DNA molecules which are homologous or at least 75% identical with them;

b) a combination of at least one DNA molecule which is shortened or not shortened in comparison with the transcribed spacer between the 23 S and 5 S genes, position 2907 to 2999 of SEQ ID NO: 1, and at least one DNA molecule which is shortened in comparison with the 5 S rDNA gene with the sequence between positions 3000 to 3112 of SEQ ID NO: 1, or DNA molecules which are homologous or at least 75% identical with them;

c) a combination of at least one DNA molecule which is shortened or not shortened in comparison with the 23 S gene with the sequence from position 2907 to 2999 of SEQ ID NO: 1, and at least one shortened DNA molecule from the 5 S rDNA gene from position 3000 to 3112 of SEQ ID NO: 1, or DNA molecules with are homologous or at least 75% identical with them;

d) a combination of at least one DNA molecule which is shortened in comparison with the 23 S gene with the sequence from position 2571 to 2906 of the SEQ ID NO: 1 and at least one shortened DNA molecule from the 5 S rDNA gene from position 3000 to 3112 of SEQ ID NO: 1, or DNA molecules which are homologous or at least 75% identical with them;

e) a combination of 2 nucleic acid molecules according to Claim 75; and

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f) a combination containing at least one DNA molecule which hybridizes with a region hybridizing at least 100 nucleotides upstream from the 3' end of the 23 S rDNA, therefore within the 23 S rDNA;

wherein the combination according to any of a) to f) can also be a combined DNA molecule comprising at least 15 base pairs, for detection of bacteria or phylogenetic groups of bacteria.

91. (Currently Amended) The method of claim ~~Method for detecting bacteria in an analytical sample according to Claim~~ 90, wherein the bacteria are enterobacteria.

92. (Currently Amended) A method ~~Method~~ for amplifying bacterial DNA of a multiplicity of different taxonomic units, especially genera and species, using primers ~~according to Claim 75~~, in which in a first amplification step the DNA for high taxonomic units such as classes, phyla or families is amplified with conserved primers, and, optionally, in at least one further amplification step (EN) parts of the first amplification fragment which are specific for genera or species can be multiplied with nested, increasingly variable primers, and, optionally, in a further step, the DNA fragments obtained by amplification which are specific for genera or species are detected by means of probes, wherein the primers used comprise nucleic acids selected from:

a) nucleic acid molecules comprising at least one sequence with any of the SEQ ID NOs: 1 to 530 and/or a sequence from position 2667 to 2720, 2727 to 2776, 2777 to 2801, 2801 to 2832, 2857 to 2896, 2907 to 2931, 2983 to 2999 and/or 3000 to 3032 according to SEQ ID NO: 1; or nucleic acids which are homologous or at least 70% identical with them;

b) nucleic acid molecules which hybridize specifically with a nucleic acid according to a);

c) nucleic acid molecules which exhibit 70% identity with a nucleic acid according to a) or b); and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

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93. (Currently Amended) The method of claim ~~Method according to Claim~~ 92, wherein ~~characterized in that~~ the process involves a PCR amplification of the nucleic acid to be detected.

94. (Currently Amended) A method ~~Method~~ according to Claim 92, wherein ~~characterized in that~~ the process involves a Southern Blot hybridization.

95. (Currently Amended) A method ~~Method~~ for amplifying bacterial DNA of a multiplicity of different taxonomic units, especially genera and species, using primers ~~according to Claim 82~~, in which in a first amplification step the DNA for high taxonomic units such as classes, phyla or families is amplified with conserved primers, and, optionally, in at least one further amplification step (EN) parts of the first amplification fragment which are specific for genera or species can be multiplied with nested, increasingly variable primers, and, optionally, in a further step, the DNA fragments obtained by amplification which are specific for genera or species are detected by means of probes, wherein the primers used comprise a combination of at least 2 nucleic acid molecules, selected from:

a) a combination of at least one DNA molecule which is shortened in comparison with the sequence SEQ ID NO: 1, position 2571 to 2906, and at least one DNA molecule which is shortened or not shortened in comparison with the transcribed spacer between the 23 S and 5 S genes corresponding to position 2907 to 2999 in SEQ ID NO: 1, or DNA molecules which are homologous or at least 75% identical with them;

b) a combination of at least one DNA molecule which is shortened or not shortened in comparison with the transcribed spacer between the 23 S and 5 S genes, position 2907 to 2999 of SEQ ID NO: 1, and at least one DNA molecule which is shortened in comparison with the 5 S rDNA gene with the sequence between positions 3000 to 3112 of SEQ ID NO: 1, or DNA molecules which are homologous or at least 75% identical with them;

c) a combination of at least one DNA molecule which is shortened or not shortened in comparison with the 23 S gene with the sequence from position 2907 to 2999 of SEQ ID NO: 1, and at least one shortened DNA molecule from the 5 S rDNA

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gene from position 3000 to 3112 of SEQ ID NO: 1, or DNA molecules with are homologous or at least 75% identical with them;

d) a combination of at least one DNA molecule which is shortened in comparison with the 23 S gene with the sequence from position 2571 to 2906 of the SEQ ID NO: 1 and at least one shortened DNA molecule from the 5 S rDNA gene from position 3000 to 3112 of SEQ ID NO: 1, or DNA molecules which are homologous or at least 75% identical with them;

e) a combination of 2 nucleic acid molecules according to Claim 75; and

f) a combination containing at least one DNA molecule which hybridizes with a region hybridizing at least 100 nucleotides upstream from the 3' end of the 23 S rDNA, therefore within the 23 S rDNA;

wherein the combination according to any of a) to f) can also be a combined DNA molecule comprising at least 15 base pairs, for detection of bacteria or phylogenetic groups of bacteria.

96. (New) The method of claim 86, wherein the nucleic acid molecule according to alternative c) exhibits at least 90% identity with a nucleic acid according to a) or b).

97. (New) The method of claim 86, wherein the one or more added nucleic acid molecule is modified or labeled so that it can generate a signal in analytical detection procedures which are known per se, with the modification selected from (i) radioactive groups, (ii) colored groups, (iii) fluorescent groups, (iv) groups for immobilization of a solid phase, and (v) groups which allow a direct or indirect reaction, especially using antibodies, antigens, enzymes, and/or substances with affinity to enzymes or enzyme complexes.

98. (New) The method of claim 86, wherein the one or more added nucleic acid molecule comprises at least one nucleic acid molecule selected from the group consisting of:

a) nucleic acid molecules comprising at least one sequence with any of the SEQ ID NOs: 2 and 25;

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b) nucleic acid molecules which hybridize specifically with a nucleic acid according to a);

c) nucleic acid molecules which exhibit 70% identity with a nucleic acid according to a) or b); and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

99. (New) The method of claim 86, characterized in that the one or more added nucleic acids comprise at least one nucleic acid molecule according to alternative a) that exhibits a sequence selected from SEQ ID NO: 211 and SEQ ID NO: 212.

100. (New) The method of claim 90, characterized in that the combination comprises at least one nucleic acid molecule selected from the group consisting of:

a) nucleic acid molecules comprising at least one sequence with any of the SEQ ID NOs: 2 and 25;

b) nucleic acid molecules which hybridize specifically with a nucleic acid according to a);

c) nucleic acid molecules which exhibit 70% identity with a nucleic acid according to a) or b); and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

101. (New) The method of claim 90, wherein the combination comprises at least one nucleic acid molecule according to alternative a) that exhibits a sequence selected from SEQ ID NO: 211 and SEQ ID NO: 212.

102. (New) The method of claim 92, wherein the nucleic acid molecule according to alternative c) exhibits at least 90% identity with a nucleic acid according to a) or b).

103. (New) The method of claim 92, wherein the primers used comprise at least one nucleic acid molecule selected from the group consisting of:

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a) nucleic acid molecules comprising at least one sequence with any of the SEQ ID NOs: 2 and 25;

b) nucleic acid molecules which hybridize specifically with a nucleic acid according to a);

c) nucleic acid molecules which exhibit 70% identity with a nucleic acid according to a) or b); and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

104. (New) The method of claim 92, wherein the primers used comprise at least one nucleic acid molecule according to alternative a) that exhibits a sequence selected from SEQ ID NO: 211 and SEQ ID NO: 212.

105. (New) The method of claim 95, wherein the primers used comprise at least one nucleic acid molecule selected from the group consisting of:

a) nucleic acid molecules comprising at least one sequence with any of the SEQ ID NOs: 2 and 25;

b) nucleic acid molecules which hybridize specifically with a nucleic acid according to a);

c) nucleic acid molecules which exhibit 70% identity with a nucleic acid according to a) or b); and

d) nucleic acid molecules which are complementary to a nucleic acid according to any of a) to c).

106. (New) The method of claim 95, wherein the primers used comprise at least one nucleic acid molecule according to alternative a) that exhibits a sequence selected from SEQ ID NO: 211 and SEQ ID NO: 212.

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